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249.384 Million cell updates/sec
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Gencore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                      OM protein – nucleic search, usin'g frame_plus_p2n model
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Command line parameters:
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-Q-CADEN\_Geneseq\_032802 -OFMT-fastap.-SUFFIX=ng -MIRMATCH=0.1 -LOOPCL=0
-LLST-45 -DOCALIGN=200 -THR\_SCORE\_pct -THR\_MAX=100 -THR\_MN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS Babesia microti BMNI-20 antigen sequence. BP AAV22749 standard; DNA; 1460 (first entry) 28-SEP-1998 AAV22749;

RESULT 1 AAV22749

antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis; ss. Location/Qualifiers 1..1509 /\*tag= a Babesia microti. Key 

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P-PSDB; AAY24365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babesia microti
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                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
 W09929869-A1
                                          11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                     17-JUN-1999.
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(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia microti; antigen; immunogen; diagnosis; infection; vaccine; immunity; detection; ss.
                                                                                                                                                                                        Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babesia microti antigen BMNI-20 complementary open reading frame.
                                                                                                                                                                                                                                                                                                                                                                       other tick-borne diseases (Lyme disease and ehrlichiosis) that
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                                                                                                                                                                                                                       infection and in protective vaccines
                                                                                                                                                                                                                                            Claim 8; Page 97-98; 113pp; English
 /product= antigen
                                                                                                                                      Reed SG,
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96US-0723142,
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                                                                                                                                      Houghton R, Lodes MJ,
                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                        WPI; 1998-195465/18.
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Best Local Similarity:
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                                                             01-OCT-1997;
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01-OCT-1996;
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Pred. No.:
                    EP834567-A2
                                         08-APR-1998
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The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY2438 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence encodes a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention; ds.
                                                                                                                                                                    Reed SG;
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                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 106-107; 126pp; English.
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                                                                                                                                                                    Lodes MJ,
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98WO-US26437
                                            97US-0990571
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17-MAR-2000; 2000US-0528784.
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                                                                                                                                                               Houghton R,
                                                                                                                     (MAYO-) MAYO FOUNDATION.
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                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
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at least can be used antibodies

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Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                         The sequence is that encoding a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick borne diseases (Lyme disease and chrischiosis) that have similar symptoms but require different treatments.
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Mismatches:
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                                                                                                  infection and in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (98..832)
                                                                                                                                 Claim 8; Page 43-44; 113pp; English
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WPI; 1998-195465/18.
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Best Local Similarity:
                 P-PSDB; AAW56297
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                                                                                               New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis; ss.
                                  McNeill PD;
                                                                                                                                                                                                                                                                                                                               Sequence 1460 BP; 539 A; 252 C; 283 G; 386 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
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/*tag= a
/product= antigen
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                                                                                                                                                                               Claim 1; Page 96; 118pp; English.
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                                  Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV22747/c
ID AAV22747 standard; DNA; 1820
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 (CORI-) CORIXA CORP.
                                                               WPI; 2000-686939/67.
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                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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Sleath PR;
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 Sleath PR;
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No.:
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                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that encoding a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                          Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG;
                                                                                                                                                                                                                                                                  Sequence 1820 BP; 686 A; 334 C; 398 G; 402 T; 0 other;
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Matches:
Conservative:
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          Sleath PR;
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                                                                                                                                                                                                                                                                                                                                                                    (1-1820)
                                                                                         infection and in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houghton R, Lodes MJ,
                                                                                                             Claim 8; Page 75-77; 113pp; English.
          Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  011/c
AAX90011 standard; DNA; 1820 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunity; detection; ss
          Lodes MJ,
                             WPI; 1998-195465/18.
                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                        P-PSDB; AAW56298
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          Houghton R,
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δλ
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The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88993 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. They microti infections. They microti infections. The present sequence encodes a B.microti antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babesia microti antigen BMNI-17 complementary open reading frame.
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 1820 BP; 402 A; 398 C; 334 G; 686 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1820
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Matches:
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                                                                        New isolated Babesia microti polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-794-764-195 (I-26) x AAX90011 (1-1820)
                                                                                                                      Example 1; Page 67-68; 126pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity; detection;
WPI; 1999-385612/32.
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P-PSDB; AAY24358.
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Best Local Similarity:
                       P-PSDB; AAY24353
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Sequence 1820 BP; 402 A; 398 C; 334 G; 686 T; 0 other;

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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAX24327 to AAX24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence encodes a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                       PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parasite; tick-borne illness; antigen; disease prevention; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. microti BMNI-17 antigen coding sequence SEQ ID NO: 17
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                                                                                                                        Sequence 1820 BP; 686 A; 334 C; 398 G; 402 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babesiosis; rodent
disease diagnosis;
                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides containing an antigenic portion of Babesia microliantice and DNAs encoding the Polypeptides, useful for diagnosing, treating or preventing B. microtiinfection, or for inducing protective immunity in a patient
                                                                                                                                       20
                                                                                                                             GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr
                                                                                                                                                                                                                                                                                                                                3. microti BMNI-17 antigen reverse complement SEQ ID NO: 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McNeill PD;
                                                                                                                                                                                                                                                                                                                                                      parasite; tick-borne illness; antigen; disease prevention; ds.
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                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevention and treatment of babesiosis.
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                                                                                                                                                                                                                                                       BP.
                                                                                                  US-09-794-764-195 (1-26) x AAC65094
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17-MAR-2000; 2000US-0528784.
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                                                                                                                                                                                                                                                                                                                                                          Babesiosis; rodent
                                                                                                                                                                                                                                                                                                                                                                         disease diagnosis;
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Best Local Similarity:
                                      Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B. microti MN-10/BMNI-17/BMNI-15 fusion protein cDNA SEQ ID
                                                                                                                                                                                   rodent parasite; tick-borne illness; antigen;
gnosis; disease prevention; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3402 BP; 1184 A; 615 C; 712 G; 891 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 111-112; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-794-764-195 (1-26) x AAC65120 (1-3402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton RL,
                                                     BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                   AAC65120 standard; cDNA; 3402
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139.00
100.00%
100.00%
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17-MAR-2000; 2000US-0528784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 ThrGlnGluIleCysGlu 26
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed SG, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-686939/67.
                                                                                                                                                                                                        disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                            WO200060090-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .gnment Scores:
                                                                                                                     12-FEB-2001
                                                                                                                                                                                        Babesiosis;
                                                                                                                                                                                                                                                                                                           12-OCT-2000
                                                                                                                                                                                                                                          Babesia sp.
                                                                                   AAC65120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                 AAC65120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL15763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                               B. microti MN-10/BMNI-17 fusion protein cDNA SEQ ID NO: 84
                                                                                                                                                                                                                                                                                                                                          parasite; tick-borne illness; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2001 BP; 742 A; 334 C; 462 G; 463 T; 0 other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                               disease prevention; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
US-09-794-764-195 (1-26) x AAC65095 (1-1820)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton RL,
                                                                                                                                                                                                        BP
                                                                                                                                                                                                      AAC65119 standard; cDNA; 2001
                                                                                                                        ACGCAAGAAATATGTGAA 1105
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139.00
100.00%
100.00%
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17-MAR-2000; 2000US-0528784
                                                                                                     ThrGlnGluIleCysGlu 26
                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                             Babesiosis; rodent
                                                                                                                                                                                                                                                                                                                                                               disease diagnosis;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                          12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                               Babesia sp.
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SG,

Reed

McNeill PD;

3402 26 0 0 0

(first entry)

26-MAR-2002

ThrGlnGluIleCysGlu 26

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δ g ó

ABL15763;

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pharmaceutical; gene; ss.
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Best Local Similarity:
Query Match:
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                                          WO200171042-A2
                                                                                                                                                                                                                                          interactions
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                                                                27-SEP-2001
                                                                                                                                                               Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS46442;
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AAS46442/c
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                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA sequences (ABL01840 ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 GGCGGTCCAAATACAAAAAAGCCGAAAAGGAATCAATTAACAGTAGTGCTCAACAAACG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr
          Drosophila melanogaster expressed polynucleotide SEQ ID NO 41771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster expressed polynucleotide SEQ ID NO 41768
                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 41771; 21\dot{p}p + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1760
12
2
10
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                         PWD,
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ABL15762 standard; cDNA; 6725
                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                              23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9
57.00
58.33%
50.00%
41.01%
                                          pharmaceutical; gene; ss
                                                               Drosophila melanogaster.
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347 GCCCAGGAAGTC 358
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                                                                                                                                                                                                                               2001-656860/75.
                                                                                                                                                                                    (PEKE ) PE CORP NY
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Best Local Similarity:
Query Match:
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                                                                                   WO200171042-A2
                                                                                                                                                                                                                                                                                       interactions
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Pred. No.:
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(ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour suppressor gene derived chemically modified sequence #164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 41768; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6725 BP; 2026 A; 1267 C; 1347 G; 2085 T; 0 other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
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11-JUL-2000; 2000US-0614150.
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57.00
58.33%
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Drosophila melanogaster.
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5379 GCCCAGGAAGIC 5368
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is

developmental biology; cell signalling; insecticide;

(first entry)

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New isolated nucleic acid detection reagent for detecting 1000 \text{ or more genes} from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                     Drosophila melanogaster expressed polynucleotide SEQ 1D NO 21998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 21998; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231
                                                                                                                              Drosophila; developmental pharmaceutical; gene; ss.
                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC, Adams M,
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P-PSDB; ABB65069.
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11-JUL-2000;
                                           26-MAR-2002
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ABL09172;
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  The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretracted DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences. Complementary to (Ss). The nucleic acid may be a peptide nucleic acid most peptide nucleic acid probes for detecting the cytosine methylation state form part of a set of probes for detecting the cytosine methylation state and/or single nucleide polymorphisms and also to be used in an array for analysing diseases associated with CPG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertalning genetic and/or epigenetic parameters for the diagnosis. and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the proposition or sequences and inferences serving as basis for diagnosis and care disadvantageous to patients. The present sequence is one of the proposition or proposition or proposition or proposition are disadvantageous to patients. The present sequence is one of the proposition of 
                                                                                                                                                                                                                                                                                                                                                                                                                        Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 164; 27pp; English.
                                                                                                                                                                                                                                                                                                                                     Berlin K;
                                                                                                                                                                      ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                       15-MAR-2001; 2001WO-EP02955
                                                                                                                                                     2000DE-1013847
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56.00
60.00%
55.00%
40.29%
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                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
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                    WO200168912-A2
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30-JUN-2000;
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Myers EW;

Li PWD,

2000US-191637P. 2000US-0614150.

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                             3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrThrGln 22
                                                                         Sequence 31449 BP; 9180 A; 6598 C; 6566 G; 9105 T; 0 other;
                                                                                                                                                                 Conservative:
                                                                                                                                                                                      Mismatches:
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Matches: Conservative: Mismatches: Indels:

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US-09-794-764-195 (1-26) x AAS46442 (1-6200)

Similarity:

Query Match:

Percent Similarity:

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Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on:

October 12, 2002, 18:42:28 ; Search time 1833 Seconds (without alignments) 296.830 Million cell updates/sec

139 1 GKPNTNKSEKAERKSHDTQTTQEICE 26 US-09-794-764-195 Perfect score: Seguence: Title:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

1797656 seqs, 10463268293 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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GenEmbl:\* Database :

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em\_htgo\_inv:\* 29: 30: 32:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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ID	22	AR129329	53	552	932	932	345	345	50	22	57	AX304629	69	AX304572	AC020862	291	AL645993	CEF40F8	AL445163	AC097962	AC100417	AC103259	CNS01DUL	AL354770	AC029651	AY061256		AF020051	AC015093	AP002988	AC087192	HSDJ383J4	AC021438	AC022351	AC073750	AC079569	0	88	$\overline{}$	4	AF312033	CNS06K1Y	1P	90	AX251196
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ALIGNMENTS

Babesia microti strain MN1 seroreactive antigen BMN1-20 gene, partial cds.
AF206527.1 GI:7716018

RESULT 1 AF206527 NCUS DEFINATION

ACCESSION VERSION KEYWORDS SOURCE

Babesia microti

ب

386

283 q

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/organism="unknown"
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ETSDDHEEGNGKLNTNKSEKTERKSHDTQTPQEIYEELGHDKINKLTAQEIYEERKEGHG
KPNTRKSEKABREKHTOKTYGEICEECEEGHDKINKNKSGNAGIKSYDTQTPQETSD"
252 c 283 g 386 t
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Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
Compounds and methods for the diagnosis and treatment of B. microti
                                                                                                                                                                   2 (bases 1 to 1460)
Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H..
Direct Submission
Submitted (18-NOV-1999) Corixa Corporation, 1124 Columbia Street,
Suite 200, Seattle, WA 98104, USA
                                         [ (bases 1 to 1460)
Lodes,M.J., Houghton,R.L., Bruinsma,E.S., Mohamath,R.,
Reynolds,L.D., Benson,D.R., Krause,P.J., Reed,S.G. and Persing,D.H.
Serological expression cloning of novel immunoreactive antigens of
Babesia microti
Infect. Immun. 68 (5), 2783-2790 (2000)
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                Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
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/organism="Babesia microti"
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Location/Qualifiers
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AR129329
AR129329.1 GI:14116991
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 Babesia microti
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AF206526 1820 bp DNA linear INV 08-MAY-2000 Babesia microti strain MN1 seroreactive antigen BNN1-17 gene, partLal cds; and seroreactive antigen BNN1-17B gene, complete cds. AF206526.1 GI:7716015
                                                                                                                                                                                                                                                        PAT 30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                          1 (sites)
Reed,S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., Mcneill,P.D.,
Homer,M.J. and Secrist,H.
Compounds and methods for the diagnosis and treatment of Babesia
microti infection
Patent: WO 0185947-A 51 15-NOV-2001;
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252 c 283 g 386 t
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Matches:
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EBCHDKINKNKSGNAGIKSYDTOTOEICEECEEGHDKINKNKSGNAGIKSYDTOP
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                                                                                                                                                                                                                    Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.
Burnolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.
Submitted (18-Nov-1999) Corixa Corporation, 1124 Columbia Street,
Suite 200, Seattle, WA 98104, USA
Location/Qualifiers
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SVTCFLRCLSIIŘFYSSISTFILIDFVMPFFTLFTYFLRCLSIIRFYSSISTFILIDF
                                                                                1 (bases 1 to 1820)
Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.
Serological expression cloning of novel immunoreactive antigens of
Babesia microti
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/note="transmembrane-region site"
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Matches:
Conservative:
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/organism="Babesia microti"
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                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5868"
632. .>1820
                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                      /strain="MN1"
                           Babesia microti
Eukaryota, Alveolata,
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ThrGlnGluIleCysGlu 26

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1 (bases 1 to 1820)
Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
Compounds and methods for the diagnosis and treatment of B. microti
PAT 16-MAY-2001
                                                                                                                          B. microti
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Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
Compounds and methods for the diagnosis and treatment of
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Location/Qualifiers
1. .1820
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AR129323 1820 bp Sequence 17 from patent US 6183976.
AR129323
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334 c 398 g
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398 c 334 g
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                                     AR129323.1 GI:14116985
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PAT 30-NOV-2001
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Reed,S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., Mcneill,P.D.,
Homer,M.J. and Secrist,H.
Compounds and methods for the diagnosis and treatment of Babesia
microtti infection
Patent: WO 0185947-A 17 15-NOV-2001;
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Reed,S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., Mcneill,P.D.,
Homer,M.J. and Secrist,H.
Compounds and methods for the diagnosis and treatment of Babesia
microti infection
Patent: WO 0185947-A 37 15-NOV-2001;
                                                       Babesia microti.
Babesia microti
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
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a 398 334 9 686 t
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                                    US-09-794-764-195 (1-26) x AR173459
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Unclassified.
1 (bases 1 to 1820)
Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
Reed, S.G. and methods for the diagnosis and treatment of B. microti infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1820)
Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
Compounds and methods for the diagnosis and treatment of B. microti
Infection
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ARI73459
ARI73459.1 GI:17913779
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Sequence 17 from patent US 6306396.
AR173458 GI:17913778
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/organism="unknown"
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1 (sites)
Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., Mcneill, P.D., Homer, M.J. and Secrist, H.
Compounds and methods for the diagnosis and treatment of Babesia microti infection
Patent: WO 0185947-A 143 15-NOV-2001;
                                                            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
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Mismatches:
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/db_xref="taxon:35084"
1 343 c 472 g 4
                                                                                                                                                        CORIXA CORPORATION (US)
Location/Qualifiers
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              GI:17383934
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Hondon, R.L., Sleath, P.R., Mcneill, P.D., Homer, M.J. and Secrist, H. Compounds and methods for the diagnosis and treatment of Babesia microti infection

Patent: WO 018547-A 84 15-NOV-2001;

CORIXA CORPORATION (U.S.)
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Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
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/organism="Babesia microti"
/db_xref="taxon:5868"
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/organism="Babesia sp."
/db_xref="taxon:35084"
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CORIXA CORPORATION (US)
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Reed.S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., Mcneill,P.D.,
Reed.S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., Mcneill,P.D.,
Compounds and methods for the diagnosis and treatment of Babesia
microti infection
Patent: WO 0185947-A 210 15-NOV-2001;
CORIXA CORPORATION (US)
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
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COMMENT
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Mus musculus clone RP23-248G14, WORKING DRAFT SEQUENCE, 52
unordered pieces.
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Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Sciurognathi; Muridae; Murinae; Mus
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Reed,S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., Mcneill,P.D.,
Homer,M.J. and Secrist,H.
Compounds and treatment of Babesia
microti infection
Patent: WO 0185947-A 86 15-NOV-2001;
CORIXA CORPORATION (US)
                      GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
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Sequence 86 from Patent WO0185947.
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Mammalia, Eutheria; Rodentia,
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DOE Joint Genome Institute.
Sequencing of Mouse
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HTG; HTGS_PHASE1; HTGS_DRAFT
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DOE Joint Genome Institute.
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Web site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 131466 bases at least Q40
Consensus quality: 172522 bases at least Q30
Consensus quality: 172522 bases at least Q20
Estimated insert size: 200094; sum-of-contigs estimation
Estimated insert size: 194000; pulse field gel estimation
Quality coverage: 3.14x in Q20 bases; pulse field gel estimation
Quality coverage: 3.05x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
29, 2000 this sequence version replaced gi:6686446
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            -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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bp in length bp in length

length length

unknown of 1982

contig contig

gap of

gap of

unknown of 1823

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14234: contig of 7713 bp in length 152949: contig of 1713 bp in length 152949: contig of 10615 bp in length gap of unknown length 161984: contig of 9035 bp in length gap of unknown length 171417: contig of 9433 bp in length gap of unknown length 185089: contig of 13672 bp in length gap of unknown length
                        contig of 1455 bp in length
gap of unknown length
contig of 1968 bp in length
gap of unknown length
contig of 2008 bp in length
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contig of 5887 bp in length
gap of unknown length
contig of 7018 bp in length
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contig of 7117 bp in length
gap of unknown length
contig of 5490 bp in length
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bp in length
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of 5020 bp in length
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contig of 8924 bp in length
gap of unknown length
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Location/Quallfiers

1. 200094

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RP23-248G14"

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151 others 200094 Length:
Matches:
Conservative:
Mismatches: 75.3 68.00 69.57 56.52 48.92 Score:
Percent Similarity;
Best Local Similarity:
Query Match:
DB: 57012 Alignment Scores: Pred. No.: BASE COUNT ORIGIN

US-09-794-764-195 (1-26) x AC020862 (1-200094)

Indels:

Db 47997 GGAAGACAGAATACAGAAAAGAAGGAAAAACAGAAACAAAGAAGAAACAAAACAAAACAAAAGA 47938 1 GlyLysProAsnThrAsnLysSekGluLysAlaGluArglysSerHisAspThrGlnThr 20 ð

21 ThrGlnGlu 23 οy

47937 ACACAAGAA 47929

Search completed: October 12, 2002, 21:54:14 Job time : 1845 secs

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Sequence 6, Appli Sequence 3, Appli Sequence 14, Appl Sequence 14, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

205, App 41, Appl

Sequence 20 Sequence 41 Sequence 3 Sequence 5 Sequence 5

Sequence Sequence Sequence Sequence Sequence

Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence Sequence

Sequence

Sequence

Sequence Sequence Sequence

Total number

Searched:

OM protein

Run on:

Sequence:

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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
US-08-471-613-15
PCT-US33-10443-15
US-08-841-349-3
US-08-841-349-3
US-08-841-349-5
US-08-841-349-5
US-08-841-349-5
US-08-841-349-5
US-08-877-353A-14
US-09-185-160-8
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US-09-185-429-1
US-08-972-927-5
US-08-996-621-1
US-09-138-930-35
US-09-138-930-35
US-09-390-020-3
US-09-390-020-3
US-08-254-358A-2
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US-08-484-956-2
US-08-757-653-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: *...
ATTORNEY/AGENT INFORMATION:
NAME: MAKi, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, Application US/08845258 Patent No. 6183976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206)682-6031 INFORMATION FOR SEQ ID NO:
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STREET: bov.
CITY: Scattle
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12, Appl
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163.756 Million cell updates/sec
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  Gençore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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US-08-990-571-51

US-08-845-258-17

US-08-990-571-17

US-08-990-571-17

US-08-990-571-17

US-08-91-142A-17

US-09-155-95-12

US-09-356-952-12

US-08-222-12

US-08-222-12

US-08-222-12
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                          October 12, 2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
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Database

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Result ٠ ي

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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Aleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRATE: Washington
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
      0000
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Matches:
Conservative:
Mismatches:
Indels:
      Conservative:
                                                                                     US-09-794-764-195 (1-26) x US-08-990-571-51 (1-1460)
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                      Mismatches:
                                       Indels:
                                                                                                                                                                                                                                                                                    Sequence 17, Application US/08845258; Patent No. 6183976; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                       (206) 622-4900
   100.00%
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Percent Similarity:
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TELEFAX: (2
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US-08-845-258-17
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                                                                                                                                                                                                                                                       RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF E
NUMBER OF SEQUENCES: 79
CORRESPONDENCE AND BERRY
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                    1460
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MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                     US-09-794-764-195 (1-26) x US-08-845-258-51 (1-1460)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/FOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPAK: (206) 622-4900
TELEFAK: (206) 622-4900
INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 51, Application US/08990571
; Patent No. 6214971
                                                                                  ; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Babesia Microti
US-08-845-258-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                   Babesia Microti
                                                                                                                                                                                  4,3e-15
139.00
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                 LENGTH: 1460 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1460 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     21 ThrGlnGluIleCysGlu 26
     SEQUENCE CHARACTERISTICS
                                                                      linear
                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                  TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104
                                                                                                                                                                    Alignment Scores:
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Predamo.:
Score:
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                                                                                                                                                                                    Pred. No.:
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Sequence 37, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/990,571

FILING DATE: 11-DEC-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MAKY, DAVIG J.

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

RECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-794-764-195 (1-26) x US-08-990-571-17 (1-1820)
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Indels:
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                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (206) 622-4900
(206)682-6031
   SEED AND BERRY
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ThrGlnGluIleCysGlu 26
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STREET 6000
CITY: Scattle
The Washington
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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Best Local Similarity:
   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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US-08-990-571-17
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US-08-990-571-37
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APPLICANT: Reed, Steven G. et al.
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath Raymond
APPLICANT: Sleath Compounce Compoun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1820
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Waki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELEPHONICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFEX: (206) 622-4900
TELEFEX: (206) 622-4900
TELEFEX: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0 v
                                                                                                                                                  Sequence 37, Application US/08645258 Patent No. 6183976 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-990-571-17/c
; Sequence 17, Application US/08990571
; Patent No. 6214971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
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Query Match:
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CITY: Se
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                                                                                              Percent Similarity:
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Query Match:
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Best Local Similarity:
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US-08-723-142A-37
         US-08-723-142A-17
                                              Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                       1820
26
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MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
COMPOTER: IRM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGBWT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPAX: (206)622-4900
TELEFAX: (206)682-6031
INFORMATION FOR EQU ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-723-142A-17/c; Sequence 17, Application US/08723142A; Patent No. 6306396; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 17:
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LENGTH: 1820 base pairs
TYPE: nucleic acid
TYPE: symplety acid
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STATE: Washington
COUNTRY: USA
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Best Local Similarity:
Query Match:
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US-08-990-571-37
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US-08-222-719-15
Sequence 15, Application US/08222719
Patent No. 5846711
GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: David D. Moore
TITLE OF INVENTION: UNCLEAR HORMONE RECEPTOR-
TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-794-764-195 (1-26) x US-08-931-999-4 (1-6755)
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
COMPUTER: IBM PS/2 Model 502 or 558X
COPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/229001
TELECOMMUNICATION INFORMATION:
    US 08/710,561
                                                                                                                      25043-A
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
STRAIN: UT0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,136
FILING DATE: 30-October-1992
CLASSIFICATION: 436
                   FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COLLINA, JOHN M.
REGISTRATION NUMBER: 26.262
REFERENCE/DOCKET NUMBER: 25043
TELECOMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFRA: 816/474-9057
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pairs
TYRE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-April-1994
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ri
                                                                                                                                                                                                                                                                                                                                unknown
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02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-931-999-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
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                                                                                                                                                                                                                                                                                              APPLICANT: Borlack Sjodin, Ann
APPLICANT: Margait, S. M.
APPLICANT: Margait, S. M.
APPLICANT: Borlack Sjodin, Dafna
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: 1999-07-19
EARLIER PAPLICATION NUMBER: 05/093,631
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER TILING DATE: 1999-07-21
NUMBER OF SEO ID NOS: 19
                          3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrThrGln 22
1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr
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US-08-931-999-4
; Sequence 4, Application US/08931999
; GENERAL INFORMATION:
; APPLICANT: Iandolo, John J.
; APPLICANT: Crupper, Scott S.
; TITLE OF INVENTION:
; WUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-794-764-195 (1-26) x US-09-356-952-12 (1-43676)
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APPLICATION NUMBER: US/08/931,999
                                                                                                                                                                                                                             Sequence 12, Application US/09356952
Patent No. 6117663
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Saccharomyces cerevisiae
                                                                                                                   1088 ACGCAAGAAATATGTGAA 1105
                                                                                           21 ThrGlnGluIleCysGlu 26
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70.00%
45.00%
38.85%
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PRIOR APPLICATION DATA:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 12
LENGTH: 43676
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US-09-356-952-12 TYPE: DNA

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Conservative: Mismatches:

Indels:

Length: Matches:

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Score:
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Patent No. 586666
GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: Jae Woon Lee
TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND
TITLE OF SEQUENCES: 31
                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                        US-09-794-764-195 (1-26) x US-08-222-719-15 (1-634)
                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
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IP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WOOTGPERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,925
FILLIG DATE: 06-June-1995
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/222,719
FILING DATE: 04-April-1994
CLASSIFICATION: 48
APPLICATION NUMBER: 07/969,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: October 30, 1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEXX: 200154
TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             54.178
37.508
33.818
                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 ACTGAATCTGTA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ThrGlnGluIle 24
                                                                                                                                                      linear
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                               LENGTH: 634
                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                    ; TOPOLOGY:
US-08-222-719-15
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1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
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                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                US-09-794-764-195 (1-26) x US-08-470-925-15 (1-634)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee
NUCLEAR HORMONE RECEPTOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFFWARE: WOTGPEFECT (Version 5.1)
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/O8/471,613
FILING DATE: 0-June-1995
CLASSIFTCATION DATA:
FILING DATE: 0-June-1994
CLASSIFTCATION NUMBER: 08/222,719
FILING DATE: 0-April-1994
CLASSIFTCATION: 436
APPLICATION NUMBER: 07/969,136
                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 4.2.
THORNEY-AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08471613 Patent No. 5962256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: October 30, 1992 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & NICHELL GIRBET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906
                                                                                                                                 17.8
47.00
54.178
37.50%
33.81%
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: David D. MOOI
APPLICANT: Jee Woon Lee
TITLE OF INVENTION: NUCI
TITLE OF INVENTION: INTE
TITLE OF INVENTION: RELA
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                   334 ACTGAATCTGTA 345
; LENGTH: 634
; TYPE: nucleic acid
; STRANDEDNESS: doub
; TOPOLGGY: linear
US-08-470-925-15
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                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                               Alignment Scores:
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Query Match:
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APPLICANT: Jae W. Lee

TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                            Matches:
Conservative:
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                                                                                                                   US-09-794-764-195 (1-26) x US-08-471-613-15 (1-634)
                                                          Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 07/969,136
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
               Length:
                                                                                                                                                                                                                                                                                                     Sequence 15, Application PC/TUS9310443 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.8
47.00
54.17%
37.50%
              17.8
47.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                             21 ThrGlnGluIle 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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02110-2804
                                          Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Alignment Scores:
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               Pred. No.:
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Sequence 6, Application US/08841349B
Patent No. 595594
Detent No. 595594
REBERAL INFORMATION:
APPLICANT: MISHRATION:
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT:
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT:
CURRENT APPLICATION NUMBER: US/08/841,349B
CURRENT APPLICATION NUMBER: US/08/841,349B
SOFTWARE: PatentIN DATE: 1997-04-30
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 6
LENGTH: 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrThrGln 22
1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1312
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5
10
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: October 12, 2002, 21:23:19
Job time: 42 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.338
37.508
33.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (402)..(1061)
US-08-841-349-6
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
                                                                                              334 ACTGAATCTGTA 345
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                                                                       21 ThrGlnGluIle 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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AQ647837 RPC193-RC
AQ647837 RPC193-BC
AQ647837 RPC193-BC
AQ6493202 T. brucei
AQ952414 Sheared D
BG753600 602733176
BIG6865 RH13201.5
BIG6865 RH13201.5
BIG6865 RH13201.5
BIG68692 RE24111.5
BIG6829 RE24111.5
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BIG678 RE5104.5
C76132 C76132 MOUS
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BIG6681 RE51058.5
BG121328 602351429
AW698464 9419 91an
AZ015973 RPCI-23-2
BF216649 601882047
BG825967 602748103
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BG337963 602435670
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BF34553 602019134
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AQ716604 HS_5467_A
                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ615735 453 bp DNA linear GSS 15-JUN-1999 HS_5143_A2_E06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=719 Col=12 Row=I, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 453)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                            BB274997 BB274997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
101 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                    AQ647837
AQ657528
AQ643134
                                                                                                                                          BI216829
BI362332
AI38922
AI512800
AA44040
BI165736
BI215736
BI271963
BI371963
BI365655
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BE305924
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BG825967
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BI243210
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BF345553
BF184134
                                                                                         AQ952414
BG753600
                                                                                                                   BI162558
BG145736
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DEFINITION
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COMMENT
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AQ615735
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BJ124088 BJ124088
                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal, to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                       27472414
         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd

    nucleic search, using frame_plus_p2n model

                                                                                                                                                                                      13736207 seqs, 6748477542 residues
                                                                                                                                                                                                       of hits satisfying chosen parameters:
                                                                                                                  26
                                                                                                                 1 GKPNTNKSEKAERKSHDTQTTQEICE
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BJ124088
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                                                             2002, 18:42:27
                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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139
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length: 200000000
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em_gss_hum:*
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em_htc:*
gb_est1:*
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Perfect score:
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Maximum DB
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Homo sapiens
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174 GTCTGCGAG 182
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Best Local Similarity:
Query Match:
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                                                                                                                        268
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                                                                                                                      BASE COUNT
ORIGIN
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BG121328
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                 g
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Clone="Piate=719 Col=12 Row=I"
// Clone=lib="RPCI-11 Human Male BAC Library"
// Sex="maile"
// Note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
// Note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
// Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
112 c 109 g 68 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.

Est.
Caenorhabditis elegans
Ebkaryota; Metrazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Bukaryota; Metrazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.

E 1 (bases 1 to 771)

St Kohara, Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
A complementary view of the C.elegans genome
AL (Dpublished (2002)
Contact: Tadasu Shin-i
Center Por Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshiniegenes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ124088 unpublished oligo-capped cDNA library, C. elegans Ll stage Caenorhabditis elegans cDNA clone ykl307d03 5', mRNA sequence.
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong uned.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
SAG primer: SPG
Class: BAC ends
High quality sequence stop: 453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
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56.00%
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BG121328 1321 bp mRNA linear EST 30-JAN-2001 602351429F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4449870 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="Index:1449870"
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Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                 J.
                                                                                                                                                                                                                                                                              5 ThrAsnLysSerGluLys---AlaGluArgLysSerHisAspThrGlnThrThrGlnGlu 23
/clone="yk1307d03"
/clone_lib="unpublished oligo-capped cDNA library,
elegans Ll stage"
/sex="hermaphrodite"
                                                                                      2 others
                                                                                                                                             771
12
5
5
1
                                                                                                                                                                          Conservative:
Mismatches:
                                                      /tissue_type="whole animal"
/dev_stage="L1"
167 c 183 q 151 t
                                                                                    151 t
                                                                                                                                                              Matches:
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                                                                                                                                                                                                        Indels:
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/db_xref="taxon:9606"
                                                                                                                                                                                                                    Gaps:
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Location/Qualifiers
1. 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BG121328
BG121328.1 GI:12614837
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60.50
73.918
52.178
43.538
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60.50
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Pred. No.:
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI, Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies).

108 c 79 g 113 t lothers
              RECI-23-290C2.TJ RPCI-23 Mus musculus genomic clone RPCI-23-290C2, AZ015973
                                                                                                                                                                                                                                                     Jacobs, Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, Jacobs, Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-290C2.TV
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhaofetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jone
Recorded-jong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Seq primer: SP6
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                                                                                                                                                                                                   Chordata;
Rodentia;
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                                                                                                                    AZ015973.1 GI:7091357
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
1 (bases 1 to 477)
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62.96%
48.15%
42.45%
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                                                                                                                                                                                                                                                              AUTHORS
    RESULT 5
AZ015973
                                                                                                                        VERSION
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                                                                                                                                                                                                                                                                                                                        AMBUB464 17-APR-2000 9419 glandular-haired subtracted CDNA library Medicago sativa CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago sativa
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Leaf and stem"
/note="glandular-haired versus non-glandular-haired
reciprocal cDNA subtraction with CLONTECH PCR-Select cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed sequence tags subtracted in reciprocal fashion between glandular-haired and non-glandular-haired full sibs of alfalfa
                                                                                                                                                            1014 AACACCAACAAGAAGAAGAAGAAACACAAGAAGCACGAGGACTCACACACGGAGACC 1073
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/db_xref="taxon:3879"
/clone_lib="glandular-haired subtracted cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, GAPRC, PSERU; Department of Agronomy Kansas State University
Throckmorton Hall, Manhattan, KS 66506, USA
Tel: 785 532 7116
Fax: 785 532 6167
Email: dhays@qenes.alfalfa.ksu.edu
Seq primer: SP6.
Location/Qualifiers
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112
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Matches:
Conservative:
Mismatches:
Indels:
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    Conservative:
Mismatches:
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                                         indels:
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Hays, D. and Skinner, D.
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52.17%
43.17%
70.83%
54.17%
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10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago sativa.
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107 æ-

Conservative: Mismatches: Indels: Matches: Length:

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BB274997
BB274997.1 GI:8972018
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59.00
72.73%
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                                         Homo sapiens
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                   human.
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/organism="Homo sapiens"
/do_xref="texon:9606"
/clone="InAGE:405539"
/clone=lib="NIH_MGC_57"
/tissue_type="glioblastoma"
/tab_host="Hil0B (TI phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGCCC-3' and 3' adaptor sequence: 5'-CACGGCATTATGCCC-3' and 3' adaptor sequence: 5'-CACGGCATTATGCCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGAGGCGGGCGCATG-TG(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 707)

E 1 (bases 1 to 707)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 164.

Location/Qualifiers
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BG825967
BG825967.1 GI:14173554
                 BF216649 107 bp mRNA linear EST 06-NOV-2000 601882947F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095539 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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                                                     mRNA sequence.
BF216649
BF216649.1 GI:11110235
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VERSION
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KEYWORDS
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/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/hab_host="nH108 (phage-resistant)"
/note="Organ: muscle; Vector: poTB7; Site_1: EcoR1;
Site_2: Xho1; cDNA made by oligo-dT priming.
Site_2: Aho1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGGAGGAG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 07-JUL-2000
                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: gapbs-remail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Conne distribution information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1795 row: e column: 02
High quality sequence stop: 541.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 338)
Ronno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 bp mRNA linear EST 07-JUL-2
BB274997 RIKEN full-length enriched, 10 days neonate cortex Mus
musculus cDNA clone A830090L18 3', mRNA sequence.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleoston Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 763)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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us-09-794-764-195.rst

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250 CCAAATCCAACAAATAGGACTAAAGGTGTAGAAAGGGAACAGCACGAAGCTTCCCACAGC 191
                                               3 ProAsn---ThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrThr 21
          US-09-794-764-195 (1-26) x BB274997 (1-338)
                                                                                                                                                                 190 CAAGAGATCTGC 179
                                                                                                                            GlnGluIleCys 25
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                                                                                                                                                                                                                                                                                                                                                            Email: genome-resegas.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,F., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyoswa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
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Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Research (RIKEN) 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Conservative:
Mismatches:
Indels:
Gaps:
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Bohui Zhao in Pieter de Jong's laboratory (Roswell Park
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brucei TREU927/4 GUTat lo.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII
segment). High molecular weight fragments were ligated in
pBACe3.6 vector digested with Eco RI or Bam HI,
respectively. The average insert size is 141 Kb. Total
coverage (both segments): > 90 X the haploid
non-minichronosomal genome."
AQD4/837
RPCI93-ECORI-1122.TV RPCI93-ECORI Trypanosoma brucei genomic clone
RPCI93-ECORI-1122, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           , Fraser, C. and Adams, M.
Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
Library for gene discovery and sequence-ready map construction
Unpublished (1999)
                                                                                                                                                                                                                                                                                                              1 (bases 1 to 589)
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gel-Sayed, N., Zhao, S., Dao, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Najib M. El-Saydad
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Enail: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
Class: BAC ends.
                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Mismatches:
Indels:
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Best Local Similarity:
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3 ProAsnThrAsnLysSerGluLysAlaGluArgLys---SerHisAspThrGlnThrThr 21
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Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                     Sheared DNA-24M10.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-24M10, DNA sequence.
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1 (bases 1 to 594)

1 (bases 1 to 594)

El-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Uilu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Perser, C. and Adams, M.

Determination of Clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
Unpublished (1999)
Other_GSSS: Sheared DNA-24M10.TF
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: MI3-Reverse
class: shotgun.
                                       ProAsnThrAsnLysSerGluLysAlaGluArgLys---SerHisAspThrGlnThrThr 21
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Press, 1999)."
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AQ657528.1 GI:5165296
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AQ657528/c
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/note="Vector: pBAC63-6; Site=1: Eco RI; Site=2: Eco RI;
/note="Trec193-EcoRI"
/note="Trec193-Trypanosoma brucei TreU927/4 GUTat 10.1 agarose embedded DNA was partially digested with a combination of Eco RI and Eco RI methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII segment). High molecular weight fragments were ligated in pBAC63.6 vector digested with Eco RI or Bam HI, respectively. The average insert size is 141 Kb. Total coverage (botts segments): > 90 X the haploid non-minichromosomal genome."

71 a 165 c 133 g 141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library for gene discovery and sequence-ready map construction

Unpublished (1999)

Other_CSSS: REC193-ECORI-6J16.TJ

Cohtact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Email: nelsayed@tigr.org

Clones and high density filters may be purchased from BACPAC

Resources (http://bacpac.med.buffalo.edu. BAC end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.

Seg primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                     AQ643134 610 bp DNA linear GSS 08-JUL-1999
RPC193-ECORI-6J16.TV RPC193-ECORI Trypanosoma brucei genomic clone
RPC193-ECORI-6J16, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 610)
El-Sayed,N., Zhao, B., Gill,S., Suh,E., Malek,J., Fujii,C., Gertrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.
Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
3 ProAsnThrAsnLysSerGluLysAlaGluArgLys---SerHisAspThrGlnThrThr 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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1. .610
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AQ643134.1 GI:5119844
                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei.
Trypanosoma brucei
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58.50
70.83%
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42.09%
                                                                                                                                      338 AATGACTGCTGC 327
                                                                                22 GlnGluIleCys 25
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22

TA340G03Q

RESULT 12

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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/organism="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/db_xref="taxon:5691"
/dlone="Sheared DNA"
/clone="Sheared Dna"
/cl
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BG753600.1 GI:14064253
                                                                                                                                                           I (bases I to 670)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujil,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ProAsnThrAsnLysSerGluLysAlaGluArgLys---SerHisAspThrGlnThrThr 2
                                                                                   Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
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Matches:
                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Other GSSs: Sheared DNA-12N24.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           indels:
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1. .670
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Press, 1999)."
a 198 c 1
     GI:6775679
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70.83%
45.83%
42.09%
                                                         brucei.
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                                                                                                                                             Trypanosoma.
                                                         Trypanosoma
  AQ952414.1
GSS.
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Best Local Similarity:
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No
                                                                                   ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                               665 bp DNA linear GSS 15-DEC-2000 genomic DNA clone 340903, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Maxing small
insert libraries for Whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr_org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hall, M., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G. Direct Submission Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
3 ProAsnThrAsnLysSerGluLySAlaGluArgLys---SerHisAspThrGlnThrThr 21
                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma brucei
Eukaryota; Euglenozod; Kinetoplastida; Trypanosomatidae;
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197 c 15
                                                                                                                                                                                                                                                                                                         genomic survey sequence
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1 (bases 1 to 665)
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                                                                             GlnGluIleCys
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Search completed: October 12, 2002, 21:22:28 Job time : 1589 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /issue__rype="normal pigmented retinal epithelium"
/lab_host="normal pigmented retinal epithelium"
/lab_host="normal pigmented retinal epithelium"
/lab_host="normal pigmented retinal"
/note="organ: eye, Vector: pormal; alte_1: XhoI: Site_2:
ECORI: cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 238)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
                                                                                        MINIMIATING TALIBETES; CATASTININI; HOMINIDAGE; HOMO.

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
(Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gappls rémail.nih.gov
Tissue Procurement: ATC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI759 row: h column: 19
High quality Sequence stop: 194.
                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RH13261.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH13261 5, mRNA sequence. B1608655 1 GI:15504180 EST.
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Indels:
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Matches:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4876482"
/clone_lib="NIH_MGC_43"
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Drosophila melanogaster
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,
Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Adult"
//lab_host="DH5-alpha TonA"
//note="Organ: head; Vector: pFlc1; Site_1: Xho1; Site_2:
//note="Organ: head; Vector pFlc1; Site_1: Xho1; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                              1. .238
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH13261"
/clone="RH Drosophila melanogaster normalized Newd
                                                                                                                                                                                Lawrence Berkeley National Lab One cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: RH.132 row: F column: 1 High quality sequence stop: 235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male and female"
                                                                                                                 Unpublished (2001)
Contact: Stapleton, M.
BDGP
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58.33%
50.00%
41.01%
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Best Local Similarity:
Query Match:
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